

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/533,144B  
Source: IFW  
Date Processed by STIC: 2/8/07

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 02/08/2007

PATENT APPLICATION: US/10/533,144B

TIME: 11:07:57

Input Set : E:\seqlist.txt

Output Set: N:\CRF4\02082007\J533144B.raw

```

4 <110> APPLICANT: MASUDA, ESTEBAN
6 <120> TITLE OF INVENTION: METHODS OF SCREENING CYCLIC PEPTIDES AND
7 IDENTIFYING TARGETS THEREFOR
10 <130> FILE REFERENCE: RIGL-023
12 <140> CURRENT APPLICATION NUMBER: 10/533,144B
13 <141> CURRENT FILING DATE: 2005-04-27
15 <150> PRIOR APPLICATION NUMBER: US03/27370
16 <151> PRIOR FILING DATE: 2003-08-30
18 <150> PRIOR APPLICATION NUMBER: 60/407,385
19 <151> PRIOR FILING DATE: 2002-08-30
21 <160> NUMBER OF SEQ ID NOS: 4
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1227
27 <212> TYPE: DNA
28 <213> ORGANISM: Artificial Sequence
30 <220> FEATURE:
31 <223> OTHER INFORMATION: synthetic oligonucleotide
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (1)...(1227)
37 <220> FEATURE:
38 <221> NAME/KEY: misc_feature
39 <222> LOCATION: 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171
40 <223> OTHER INFORMATION: n = A,T,C or G
42 <400> SEQUENCE: 1
43 atg gag agc ggc agc ccc gag atc gag aag ctg agt cag agc gac atc 48
44 Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile
45 1 5 10 15
47 tac tgg gac agc atg gtg agc atc acc gag acc ggc gtg gag gag gtg 96
48 Tyr Trp Asp Ser Met Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val
49 20 25 30
51 ttc gac ctg acc gtg ccc ggc ccc cac aac ttc gtg gcc aac gac atc 144
52 Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile
53 35 40 45
W--> 55 atc gtc cac aac agc nnn nnn nnn nnn tgc atc agc ggc gac agc ctg 192
W--> 56 Ile Val His Asn Ser Xaa Xaa Xaa Xaa Cys Ile Ser Gly Asp Ser Leu
57 50 55 60
59 atc agc ctg gcc agc acc ggc aag agg gtg agc atc aag gac ctg ctg 240
60 Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp Leu Leu
61 65 70 75 80
63 gac gag aag gac ttc gag atc tgg gcc atc aac gag cag acc atg aag 288
64 Asp Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr Met Lys

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65	85	90	95	
67 cta gag agc gcc aag gtg agc agg gtg ttc tgc acc ggc aag aag cta	336			
68 Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys Lys Leu				
69 100 105 110				
71 gtg tac atc cta aga acc agg cta ggc agg acc atc aag gcc acc gcc	384			
72 Val Tyr Ile Leu Arg Thr Arg Leu Gly Arg Thr Ile Lys Ala Thr Ala				
73 115 120 125				
75 aac cac agg ttc cta acc atc gac ggc tgg aag agg cta gac gag cta	432			
76 Asn His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp Glu Leu				
77 130 135 140				
79 agc cta aag gag cac atc gcc cta ccc cgg aag cta gag agc agc agc	480			
80 Ser Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser Ser Ser				
81 145 150 155 160				
83 cta cag cta ggc ctc cgc ggc cag atc gat gtg agc aag ggc gag gag	528			
84 Leu Gln Leu Gly Leu Arg Gly Gln Ile Asp Val Ser Lys Gly Glu Glu				
85 165 170 175				
87 ctg ttc acc ggg gtg gtg ccc atc ctg gtc gag ctg gac ggc gac gta	576			
88 Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val				
89 180 185 190				
91 aac ggc cac aag ttc agc gtg tcc ggc gag ggc gag ggc gat gcc acc	624			
92 Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr				
93 195 200 205				
95 tac ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	672			
96 Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro				
97 210 215 220				
99 gtg ccc tgg ccc acc ctc gtg acc acc ctg acc cac ggc gtg cag tgc	720			
100 Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr His Gly Val Gln Cys				
101 225 230 235 240				
103 ttc agc cgc tac ccc gac cac atg aag cag cac gac ttc ttc aag tcc	768			
104 Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser				
105 245 250 255				
107 gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	816			
108 Ala Met Pro Glu Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp				
109 260 265 270				
111 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	864			
112 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr				
113 275 280 285				
115 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	912			
116 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly				
117 290 295 300				
119 aac atc ctg ggg cac aag ctt gag tac aac ttc aac agc cac aac gtg	960			
120 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val				
121 305 310 315 320				
123 tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	1008			
124 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys				
125 325 330 335				
127 atc cgc cac aac atc gag gac gga tcc gtg cag ctc gcc gac cac tac	1056			
128 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr				
129 340 345 350				

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```

131 cag cag aac acc cca att ggc gac ggg ccc gtg ctg ctg ccc gac aac 1104
132 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
133      355      360      365
135 cac tac ctg agc acc cag agc gct ctt tcg aaa gac ccc aac gag aag 1152
136 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
137      370      375      380
139 cgc gat cat atg gtc ctg ctc gag ttc gtg acc gcc gcc ggg atc act 1200
140 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
141 385      390      395      400
143 ctc ggc atg gac gag ctg tac aag taa 1227
144 Leu Gly Met Asp Glu Leu Tyr Lys *
145      405
148 <210> SEQ ID NO: 2
149 <211> LENGTH: 408
150 <212> TYPE: PRT
151 <213> ORGANISM: Artificial Sequence
153 <220> FEATURE:
154 <221> NAME/KEY: VARIANT
155 <222> LOCATION: 54, 55, 56, 57
156 <223> OTHER INFORMATION: Xaa = Any Amino Acid
158 <220> FEATURE:
159 <223> OTHER INFORMATION: synthetic polypeptide
161 <400> SEQUENCE: 2
162 Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile
163 1      5      10      15
164 Tyr Trp Asp Ser Met Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val
165      20      25      30
166 Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile
167      35      40      45
W--> 168 Ile Val His Asn Ser Xaa Xaa Xaa Xaa Cys Ile Ser Gly Asp Ser Leu
169      50      55      60
170 Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp Leu Leu
171 65      70      75      80
172 Asp Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr Met Lys
173      85      90      95
174 Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys Lys Leu
175      100      105      110
176 Val Tyr Ile Leu Arg Thr Arg Leu Gly Arg Thr Ile Lys Ala Thr Ala
177      115      120      125
178 Asn His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp Glu Leu
179      130      135      140
180 Ser Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser Ser Ser
181 145      150      155      160
182 Leu Gln Leu Gly Leu Arg Gly Gln Ile Asp Val Ser Lys Gly Glu Glu
183      165      170      175
184 Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val
185      180      185      190
186 Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr
187      195      200      205

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Input Set : E:\seqlist.txt

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```

188 Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
189      210                215                220
190 Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr His Gly Val Gln Cys
191 225                230                235                240
192 Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser
193                245                250                255
194 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
195                260                265                270
196 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
197                275                280                285
198 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
199      290                295                300
200 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val
201 305                310                315                320
202 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
203                325                330                335
204 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
205                340                345                350
206 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
207                355                360                365
208 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
209      370                375                380
210 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
211 385                390                395                400
212 Leu Gly Met Asp Glu Leu Tyr Lys
213                405
216 <210> SEQ ID NO: 3
217 <211> LENGTH: 5
218 <212> TYPE: PRT
219 <213> ORGANISM: Artificial Sequence
221 <220> FEATURE:
222 <223> OTHER INFORMATION: synthetic peptide
224 <400> SEQUENCE: 3
225 Gly Ser Gly Gly Ser
226 1 5
229 <210> SEQ ID NO: 4
230 <211> LENGTH: 4
231 <212> TYPE: PRT
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: synthetic peptide
237 <400> SEQUENCE: 4
238 Ala Gly Pro Ile
239 1

```

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/533,144B

DATE: 02/08/2007  
TIME: 11:07:58

Input Set : E:\seqlist.txt  
Output Set: N:\CRF4\02082007\J533144B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 160,161,162,163,164,165,166,167,168,169,170,171/

Seq#:1; Xaa Pos. 54,55,56,57

Seq#:2; Xaa Pos. 54,55,56,57

VERIFICATION SUMMARY

DATE: 02/08/2007

PATENT APPLICATION: US/10/533,144B

TIME: 11:07:58

Input Set : E:\seqlist.txt

Output Set: N:\CRF4\02082007\J533144B.raw

L:55 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:144

L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:192

L:168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:48